## Analysis of Functional Magnetic Resonance Imaging (fMRI)

# Image Preprocessing

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## Teaching Materials

- http://www.ym.edu.tw/~cflu/CFLu_course_fMRIana.html
- ***Week 6: Image Preprocessing of fMRI***
  ***<Handout>***Lesson6_slides.pdf
  ***<Materials>***fMRIana06_materials.zip



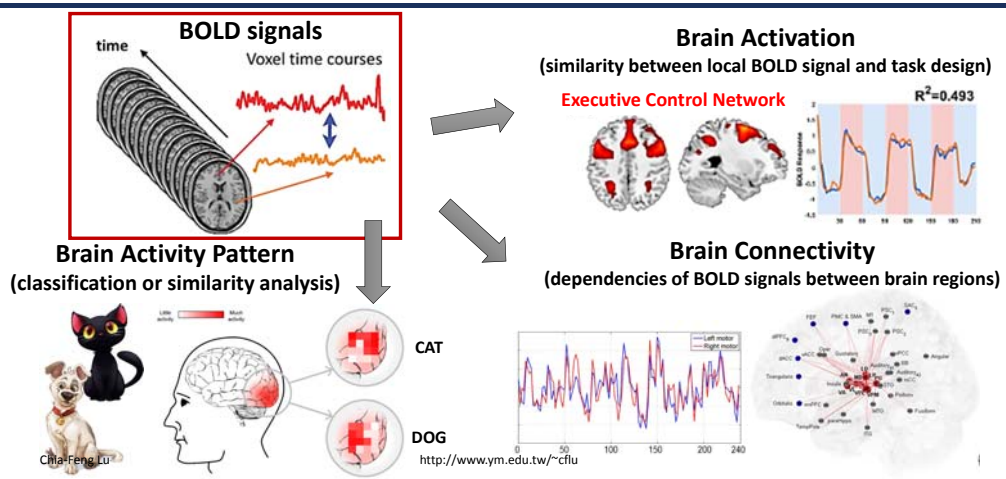
## Employed Software

- **RadiAnt DICOM Viewer**
  - https://www.radiantviewer.com/
- **MRIcro**
  - https://people.cas.sc.edu/rorden/mricro/mricro.html#Installation
  - https://www.mccauslandcenter.sc.edu/crnl/mricro
- **Statistical Parametric Mapping (SPM 12)**
  - http://www.fil.ion.ucl.ac.uk/spm/

**[Caution] File name\path contains Chinese character or space may cause error!**

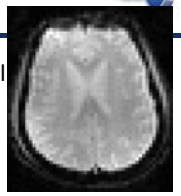


## fMRI Analysis

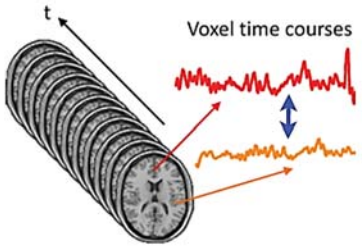


# fMRI Protocol

- Siemens 3T MAGNETOM Trio Scanner @ NYMU, 32-channel head coil
- Single-Shot 2D EPI (GRE-EPI), T2* weighting
- Repetition Time = 2000 ms
- Echo Time = 20 ms
- Flip Angle = 70~90°
- NEX = 1
- Slice thickness = 3.4 mm
- Field of View = 220 x 220 mm²
- Matrix size = 64 x 64
- Slice number = 40
- Volume number **(depends on experiment design)**



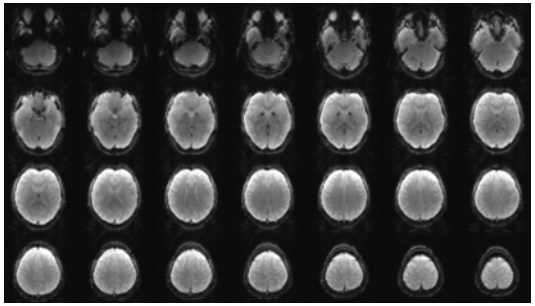
**3.44 x 3.44 x 3.40 mm³**





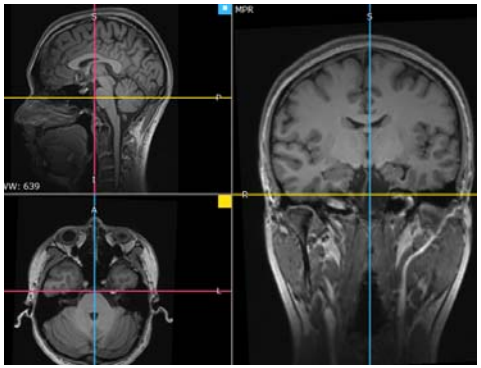

# Acquired Data

**BOLD EPI images (mosaics)**



**Cropped, slice number = 40**

**MPRAGE 3D T1W images**

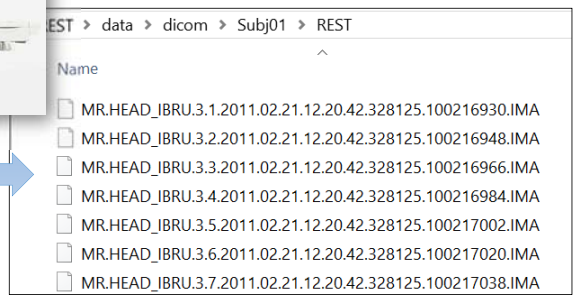




# Let's Start from Very Beginning

**Siemens 3T Trio Scanner @NYMU**

**DICOM format (*.dcm, *.ima)**
⇔ **NIfTI (.nii)** or Analyze75 (*.hdr, *.img)






# DICOM (1993)

- **D**igital **I**maging and **CO**mmunication in **M**edicine

DICOM
Digital Imaging and Communications in Medicine

NEMA, Suite 1752
1300 North 17th Street
Rosslyn, VA 22209
Ph: (703) 841-3285
http://dicom.nema.org

http://dicom.nema.org/

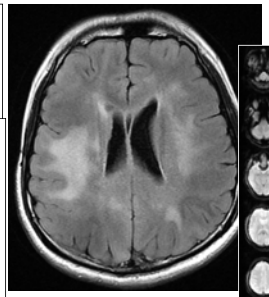
**"The Common Language of Medical Equipment"**

- ACR & NEMA formed a committee in 1983
  - American College of Radiology
  - National Electrical Manufacturers Association

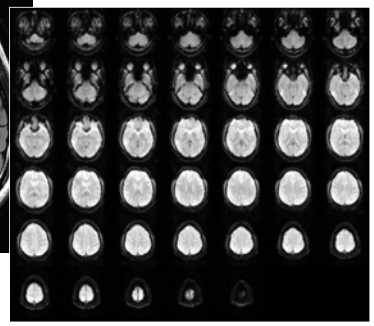
# DICOM format

**Header** + **Image data**

0008,0020,Study Date=20151204
0008,0021,Series Date=20151204
0008,0022,Acquisition Date=20151204
0008,0023,Image Date=20151204
0008,0030,Study Time=122630
0008,0031,Series Time=122800
0008,0032,Acquisition Time=122800
0008,0033,Imag
0008,0050,Acq
0008,0060,Mod
0008,0070,Man
0008,0080,Insti
0008,0090,Refe
0008,1010,Stati
0008,1030,Stud
0008,103E,Seri
0008,1070,Ope
0008,1090,Man
0018,0050,Slice Thickness=5
0018,0080,Repetition Time [TR, ms]=8002
0018,0081,Echo Time [TE, ms]=127.948
0018,0082,Inversion Time=2000
0018,0083,Number of Averages=1
0018,0084,Imaging Frequency=63.854903
0018,0085,Imaged Nucleus=1H
0018,0086,Echo Number=
0018,0087,Magnetic Field Strength=1.5
0018,0088,Spacing Between Slices=6
0018,0091,Echo Train Length=1

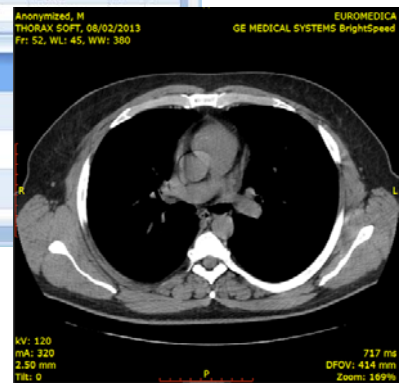


**Mosaics**



Retrieve of subject/imaging information.
**Use with caution! Personal privacy!**



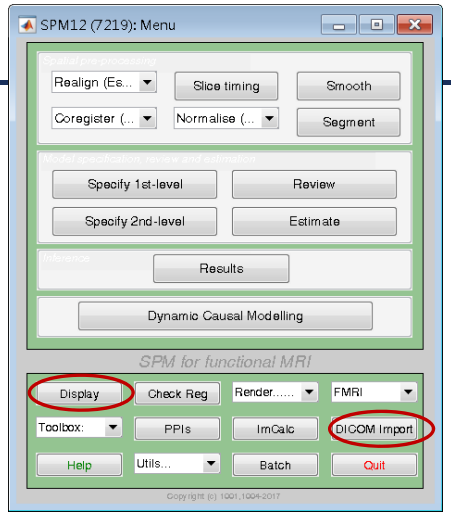



- Data query
- Image Information
- Communication

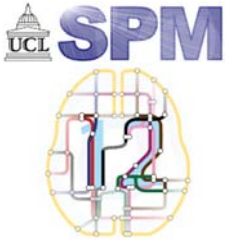


# DICOM Import

**Switch current directory to data folder in MATLAB.**
It is convenient for the subsequent data selection.



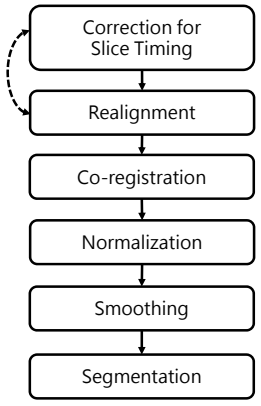

**2. Check converted images**
**(or check images by MRIcro)**



**1. Convert DICOM to NIfTI files**
**(MPRAGE, 1BACK, 2BACK)**



# Preprocessing Procedure




**Files to be created.**

a*.nii

ra*.nii, mean*.nii, rp_*.txt

The same filename with modified header.

wra*.nii, w*.mat

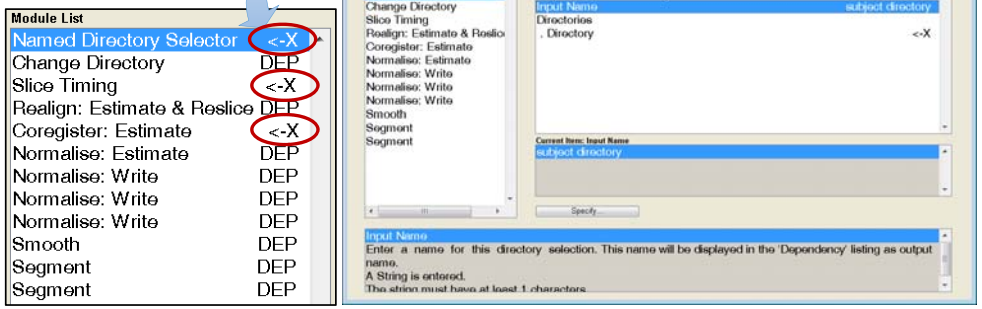
swra*.nii

c1*.nii, c2*.nii, c3*.nii mws*.nii, BiasField_*.nii

# Batch of SPM fMRI preprocessing

>> spm fmri → Batch

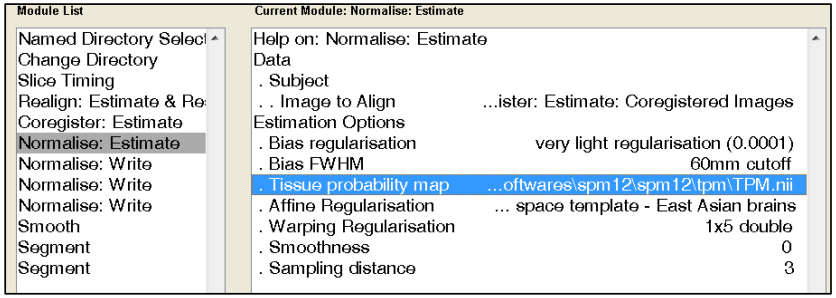
**Batch_fMRIpreproc.mat**






# Batch of SPM fMRI preprocessing

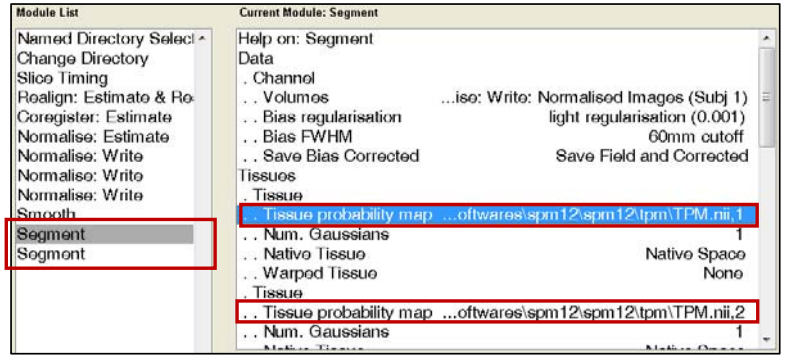
**Reselect the SPM Tissue Probability Map (TPM.nii).**






# Batch of SPM fMRI preprocessing

**Reselect the SPM TPM.nii and save your own batch template.**



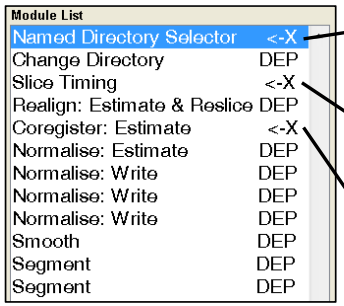

**TPM.nii,1**
**TPM.nii,2**
**TPM.nii,3**
**TPM.nii,4**
**TPM.nii,5**
**TPM.nii,6**



# Batch of SPM fMRI preprocessing

**Select the FILES for processing**

**Taking the 1Back data as an example.**

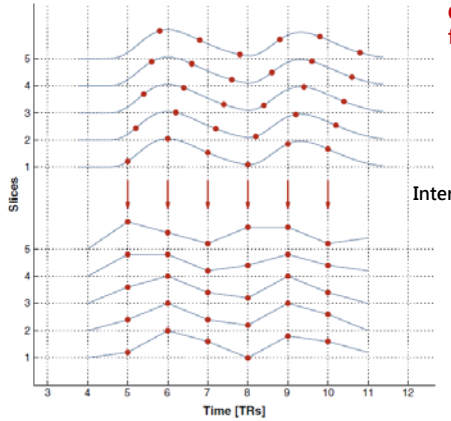



**Subject data folder**
D:\.....\fMRIana06_materials**processed\1BACK**

**fMRI data**
D:\.....\fMRIana06_materials**processed\1BACK*.nii**
....
**165 files/volumes**

**T1W data**
D:\.....\fMRIana06_materials**processed\1BACK\MPRAGE*.nii**
**1 file**

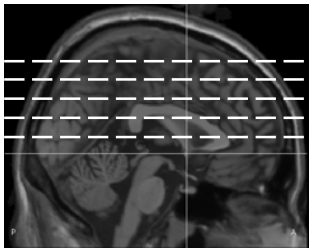
# Correction for Slice Timing




Correction for slightly different imaging timing for multi-slice acquisition in a TR.

For example:
Acquire 5 slices in 1 TR
➔ Temporal offset between slices

Interpolation



Sladky et al, NeuroImage 2011,58:588-594.



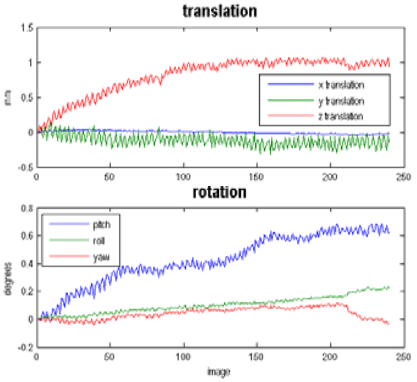
# Realignment of head motion

- **The signal variation from movement is larger than hemodynamic response.**

6-parameter Rigid body registration
& transformation (align to the 1st volume)
➔ 6 co-variates for rs-fMRI analysis

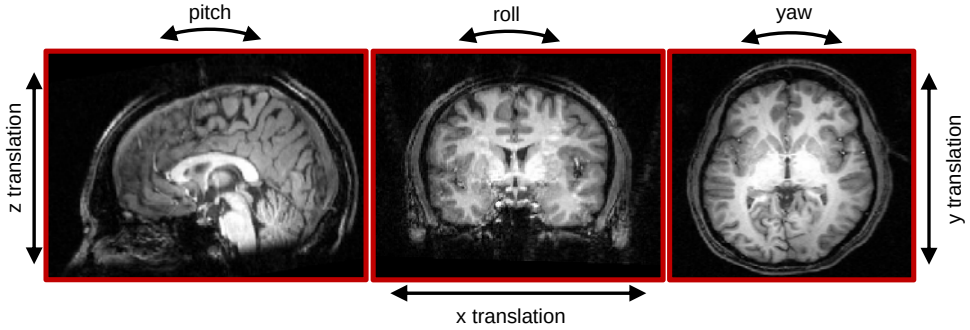
An example:








# 3 translations and 3 rotations

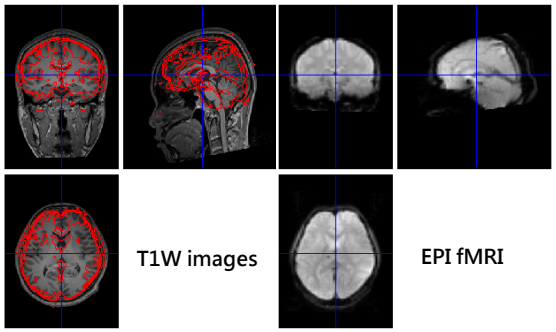



fMRI slides from http://culhamlab.ssc.uwo.ca/fmri4newbies/Tutorials.html



# Co-registration

- Align structural (T1W) images to fMRI (EPI) data.
  - Rigid body transformation using mutual information
  - Manual adjustment

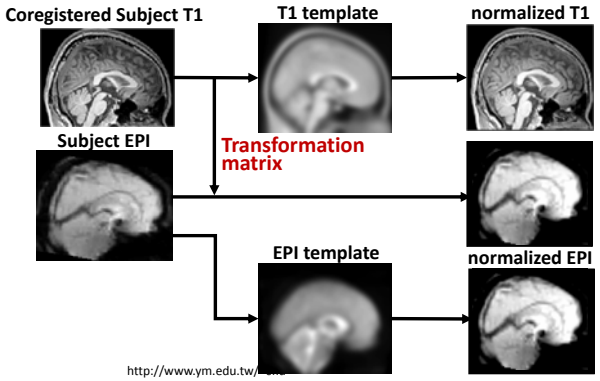


T1W images

EPI fMRI

# Spatial Normalization

- We can perform spatial normalization using either anatomical (T1) images or fMRI (EPI) data.



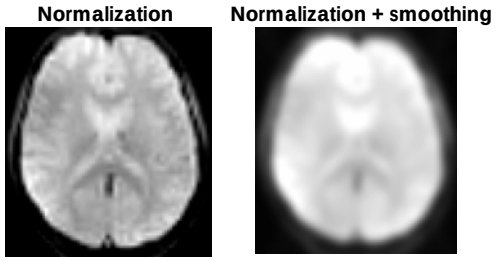



# Gaussian Spatial Smoothing

- Each voxel becomes weighted average of surrounding voxels.
- Render the data more normally distributed.
- Compensate for inaccuracies in normalization between individuals.
- Increase signal-to-noise ratio

**Smoothing process may be skipped in the certain analysis, such as MVPA.**

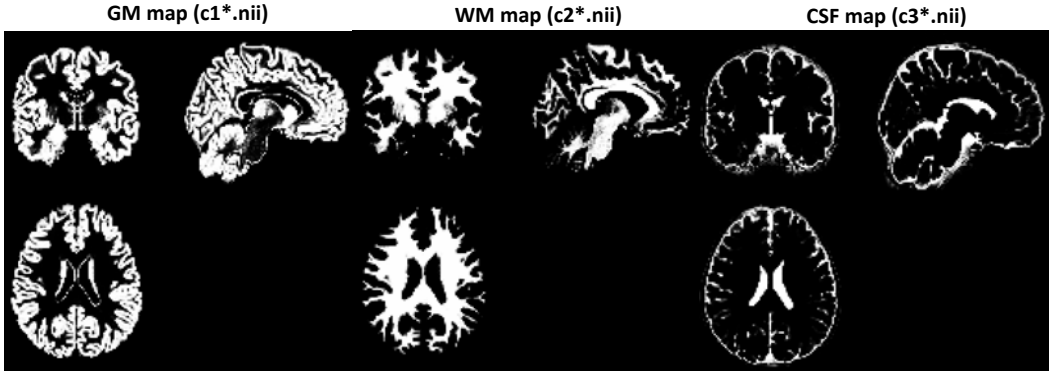
**2 x 2 x 2 mm$^3$**






# Tissue Segmentation

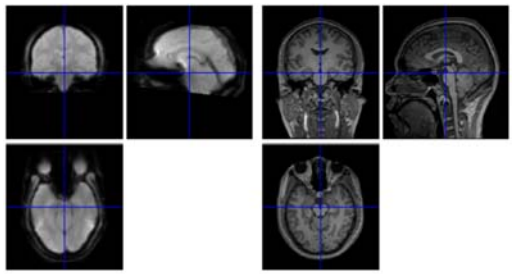
**Tissue Probability Maps**

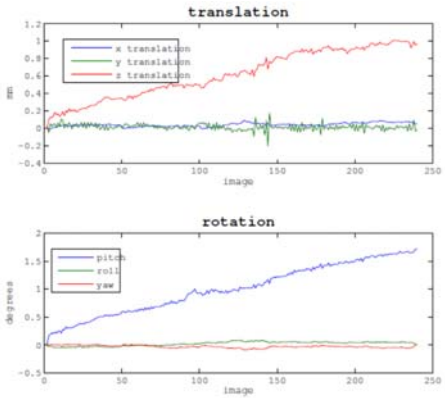





# Always Check Your Data!

- SPM processing logfile (spm_Date.ps)
- https://online2pdf.com/convert-ps-to-pdf





# THE END

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**Teaching Materials:** http://www.ym.edu.tw/~cflu/CFLu_course_fMRIana.html



## EPI undistortion/unwarp

- Magnetic inhomogeneity can cause
  - Signal loss
  - Spatial distortion
- Magnetic field warps at tissue boundaries
  - The frontal pole, orbito-frontal cortex
  - Medial temporal lobe (hippocampus)
- The benefit of undistortion/unwarp
  - Make the shape of an individual's fMRI data more similar to their anatomical images.